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Input file 17867cons; Output File 17867tra
 Sequence length 3366

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	CCCCGCGTCCGGCATGATTTAAGATTAAATTCATGTATTGAAAATATTGTTTCAGACCCCATGTGACATAAATGGAGCCA							
80	90	100	110	120	130	140	M F H	3154
	GTGCAGTGCCATGAAGAACTACGAGATTAGCCTGGATATTAACCTTGCTTCTAGAGAATAGATTTC ATG TTC CAT							
							146	
S	S	A	M	V	N	S	H	R
TCT	TCT	GCA	ATG	GTT	AAT	TCA	CAC	AGA
								23
C	L	T	A	I	L	P	Q	I
TGC	TTA	ACA	GCC	ATC	TTG	CCC	CAA	ATA
								43
Y	H	F	T	E	D	P	G	A
TAT	CAC	TTC	ACT	GAG	GAT	CCT	GGG	GCT
								63
W	Q	E	L	R	L	P	S	V
TGG	CAG	GAG	CTA	AGG	CTC	CCC	AGT	GTG
								83
P	N	L	T	S	L	D	F	V
CCC	AAT	CTC	ACC	TCT	CTG	GAC	TTT	GTT
								103
A	T	Q	F	I	L	H	S	K
GCT	ACC	CAG	TTT	ATC	ATC	TTG	CAC	AGC
								103
S	E	E	D	S	R	Y	M	K
TCA	GAG	GAA	GAT	TCA	AGA	TAC	ATG	AAA
								143
A	H	E	Q	I	A	L	L	V
GCT	CAT	GAA	CAA	ATT	GCA	CTG	CTG	GTT
								163
V	A	M	D	F	Q	A	K	L
GTG	GCT	ATG	GAC	TTC	CAA	GCC	AAG	TTA
								183
Y	R	T	L	G	G	E	T	R
TAC	AGA	ACT	CTT	GGT	GGT	GAA	ACA	AGA
								203
A	R	M	A	F	P	C	F	D
GCA	CGC	ATG	GCT	TTC	CCT	TGC	TTT	GAT
								223
I	R	R	E	S	R	H	I	A
ATA	CGA	AGA	GAG	AGC	AGG	CAT	ATT	GCA
								243
L	E	G	G	L	L	E	D	H
CTT	GAA	GGA	GGT	CTT	TTG	GAA	GAT	CAC
								263
V	A	Y	I	V	C	D	F	H
GTA	GCC	TAC	ATA	GTT	TGT	GAT	TTC	CAC
								283
V	S	I	Y	A	S	P	D	K
GTG	TCC	ATC	TAT	GCA	TCC	CCA	GAC	AAA
								303
L	K	L	L	D	F	Y	E	K
CTG	AAG	CTA	CTT	GAT	TTT	TAT	GAA	AAG
								323
D	L	I	A	I	P	D	F	A
GAT	TTA	ATT	GCT	ATT	CCT	GAC	TTT	GCA
								343
Y	R	E	T	S	L	L	F	D
TAT	AGG	GAG	ACG	TCA	CTG	CTT	TTT	GAC
								363
V	T	R	V	I	A	H	E	L
GTC	ACC	AGA	GTC	ATA	GCC	CAT	GAA	CTG
								383
								1149

FIG. 1A.

1003603-13101

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E W W N D I W L K E G F A K Y M E L I A 403
 GAA TGG TGG AAT GAT ATT TGG CTT AAG GAG GGT TTT GCA AAA TAC ATG GAA CTT ATC GCT 1209
 V N A T Y P E L Q F D D Y F L N V C F E 423
 GTT AAT GCT ACA TAT CCA GAG CTG CAA TTT GAT GAC TAT TTT TTG AAT GTG TGT TTT GAA 1269
 V I T K D S L N S S R P I S K P A E T P 443
 GTA ATT ACA AAA GAT TCA TTG AAT TCA TCC CGC CCT ATC TCC AAA CCA GCG GAA ACC CCG 1329
 T Q I Q E M F D E V S Y N K G A C I L N 463
 ACT CAA ATA CAG GAA ATG TTT GAT GAA GTT TCC TAT AAC AAG GGA GCT TGT ATT TTG AAT 1389
 M L K D F L G E E K F Q K G I I Q Y L K 483
 ATG CTC AAG GAT TTT CTG GGT GAG GAG AAA TTC CAG AAA GGA ATA ATT CAG TAC TTA AAG 1449
 K E S Y R N A K N D D L W S S L S N S C 503
 AAG TTC AGC TAT AGA AAT GCT AAG AAT GAT GAC TTG TGG AGC AGT CTG TCA AAT AGT TGT 1509
 L E S D F T S G G V C H S D P K M T S N 523
 TTA GAA AGT GAT TTT ACA TCT GGT GGA GTT TGT CAT TCG GAT CCC AAG ATG ACA AGT AAC 1569
 M L A E L G E N A E V K E M M T T W T L 543
 ATG CTC GCC TTT CTG GGG GAA AAT GCA GAG GTC AAA GAG ATG ATG ACT ACA TGG ACT CTC 1629
 Q K G I P L L V V K Q D G C S L R L Q Q 563
 CAG AAA GGA ATC CCC CTG CTG GTG GTT AAA CAA GAC GGG TGT TCA CTC CGA CTG CAA CAG 1689
 E R F L Q G V F Q E D P E W R A L Q E R 583
 GAG CGC TTC CTC CAG GGG GTT TTC CAG GAA GAC CCT GAA TGG AGG GCC CTG CAG GAG AGG 1749
 Y L W H I P L T Y S T S S N V L H R H 603
 TAC CTG TGG CAT ATC CCA TTG ACC TAC TCC ACG AGT TCT TCT AAT GTG ATC CAC AGA CAC 1809
 I L K S K T D T L D L P E K T S W V K F 623
 ATT CTA AAA TCA AAG ACA GAT ACT CTG GAT CTA CCT GAA AAG ACC AGT TGG GTG AAA TTT 1869
 N V D S N G Y Y I V H Y E G H G W D Q L 643
 AAT GTG GAC TCA AAT GGT TAC TAC ATC GTT CAC TAT GAG GGT CAT GGA TGG GAC CAA CTC 1929
 I T Q L N Q N H T L L R P K D R V G L I 663
 ATT ACA CAG CTG AAT CAG AAC CAC ACA CTT CTC AGA CCT AAG GAC AGA GTA GGT CTG ATT 1989
 H D V F Q L V G A G R L T L D K A L D M 683
 CAT GAT GTG TTT CAG CTA GTT GGT GCA GGG AGA CTG ACC CTA GAC AAA GCT CTT GAC ATG 2049
 T Y Y L Q H E T S S P A L L E G L S Y L 703
 ACT TAC TAC CTC CAA CAT GAA ACA AGC AGC CCC GCA CTT CTC GAA GGT CTG AGT TAC TTG 2109
 E S F Y H M M D R R N I S D I S E N L K 723
 GAA TCG TTT TAC CAC ATG ATG GAC AGA AGG AAT ATT TCA GAT ATC TCT GAA AAC CTC AAG 2169
 R Y L L Q Y F K P V I D R Q S V S D K G 743
 CGT TAC CTT CTT CAG TAT TTT AAG CCA GTG ATT GAC AGG CAA AGC TGG AGT GAC AAG GGC 2229
 S V W D R M L R S A L L K L A C D L N H 763
 TCA GTC TGG GAC AGG ATG CTC CGC TCG GCT CTC TTG AAG CTG GCC TGT GAC CTG AAC CAT 2289
 A P C I Q K A A E L F S Q W M E S S G K 783
 GCT CCT TGC ATC CAG AAA GCT GCT GAA CTC TTC TCC CAG TGG ATG GAA TCC AGT GGA AAA 2349
 L N I P T D V L K I V Y S V G A Q T T A 803
 TTA AAT ATA CCA ACA GAT GTT TTA AAG ATT GTG TAT TCT GTG GGT GCT CAG ACA ACA GCA 2409
 G W N Y L L E Q Y E L S M S S A E Q N K 823
 GGA TGG AAT TAC CTT TTA GAG CAA TAT GAA CTG TCA ATG TCA AGT GCT GAA CAA AAC AAA 2469

FIG. 1B.

1003903 "E206E001"

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I L Y A L S T S K H Q E K L L K L I F L 843
ATT CTG TAT GCT TTG TCA ACG AGC AAG CAT CAG GAA AAG TTA CTG AAG TTA ATT GAA CTA 2529
G M E G K V I K T Q N L A A L L H A I A 863
GGA ATG GAA GGA AAG GTT ATC AAG ACA CAG AAC TTG GCA GCT CTC CTT CAT GCG ATT GCC 2589
R R P K G Q Q L A W D F V R E N W T H L 883
AGA CGT CCA AAG GGG CAG CAA CTA GCA TGG GAT TTT GTA AGA GAA AAT TGG ACC CAT CTT 2649
L K K E D L G S Y D I R M I I S G T T A 903
CTG AAA AAA TTT GAC TTG GGC TCA TAT GAC ATA AGG ATG ATC ATC TCT GGC ACA ACA GCT 2709
H F S S K D K L Q E V K L F F E S L E A 923
CAC TTT TCT TCC AAG GAT AAG TTG CAA GAG GTG AAA CTA TTT TTT GAA TCT CTT GAG GCT 2769
Q G S H L D I E Q T V L E T I T K N I K 943
CAA GGA TCA CAT CTG GAT ATT TTT CAA ACT GTT CTG GAA ACG ATA ACC AAA AAT ATA AAA 2829
V L E K N L P T L R T V L M V N T * 961
TGG CTG GAG AAG AAT CTT CCG ACT CTG AGG ACT TGG CTA ATG GTT AAT ACT TAA 2883

ATGGTCAATAGAAAAAGTAGGCTGGGCGCGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCTGAGAAGGGCGGA
TCACGAGGTCAGGAGATGGAGACCATCCTGGCTAACACGGTGAGACCCCGTCTCCGCTAAAAATACAAAAATTAGCCG
GGCATGGTGGCAGGTGCCTGTAGTCCCAGCTACTCGGCAGGCTGCAGCAGGAAAATGGCATAAACCCGGGAGGTGGAGC
TTGCAGTGAGCCGAGATTGCACCACTGCATTCCAGCCTGGGTGACTGAGCGAGACTCTGTCTCAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIG. 1C.

FIG. 1C



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Analysis of sequence7420 (960 aa)

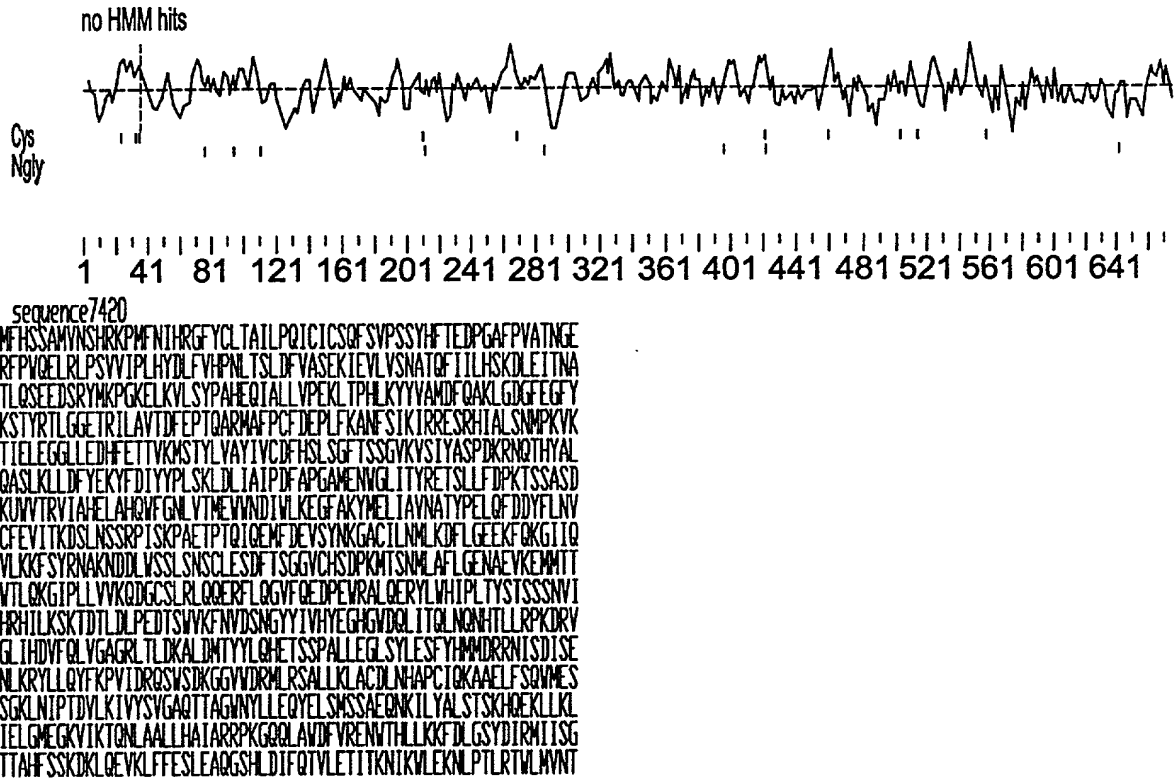


FIG. 3.

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Prosite Pattern Matches for sequence7420

>PS00001/PDOC00001/ASN_GLYCOSYLATION N-glycosylation site.

Query:	85	NLTS	88
Query:	103	NATQ	106
Query:	119	NATL	122
Query:	219	NFSI	222
Query:	294	NQTH	297

FIG. 4A.

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Query:	405	NATY	408
Query:	431	NSSR	434
Query:	650	NHTL	653
Query:	714	NISD	717
Query:	879	NWTH	882

>PS00004/PDOC00004/CAMP_PHOSPHO_SITE cAMP - and cGMP-dependent protein kinase phosphorylation site.

Query:	225	RRES	228
Query:	483	KKFS	486

>PS00005/PDOC00005/PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query:	10	SHR	12
Query:	94	SEK	96
Query:	183	TYR	185
Query:	221	SIK	223
Query:	256	TVK	258
Query:	303	SLK	305
Query:	343	TYR	345
Query:	359	SDK	361
Query:	432	SSR	434
Query:	486	SYR	488
Query:	558	SLR	560
Query:	740	SDK	742
Query:	781	SGK	783
Query:	830	TSK	832
Query:	906	SSK	908
Query:	951	TLR	853

>PS00006/PDOC00006/CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query:	57	TNGE	60
Query:	87	TSLD	90
Query:	124	SEED	127
Query:	197	TDFE	200
Query:	321	SKLD	324
Query:	343	TYRE	346
Query:	357	SASD	360
Query:	407	TYPE	410
Query:	502	SCLE	505
Query:	607	SKTD	610
Query:	701	SYLE	704
Query:	738	SWSD	741
Query:	744	SVWD	747
Query:	817	SSAE	820

FIG. 4B.

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Query: 906 SSKD 909
Query: 926 SHLD 929
Query: 933 TVLE 936

>PS00007/PDOC00007/TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.

Query: 312 KYFDIYY 318
Query: 622 KFNVDNGY 630
Query: 679 KALDMTY 686
Query: 885 KKFDLGSY 892

>PS00008/PDOC00008/MYRISTYL N-myristoylation site.

Query: 281 GVKVSI 286
Query: 334 GAMENW 339
Query: 378 GNLVTM 383
Query: 512 GVCHSD 517
Query: 798 GAQTTA 803
Query: 868 GQQLAW 873

>PS00142/PDOC00129/ZINC_PROTEASE Neutral zinc metalloproteinases, zinc-binding region signature.

Query: 367 VIAHELAHQW 376

FIG. 4C.

FIG. 4C

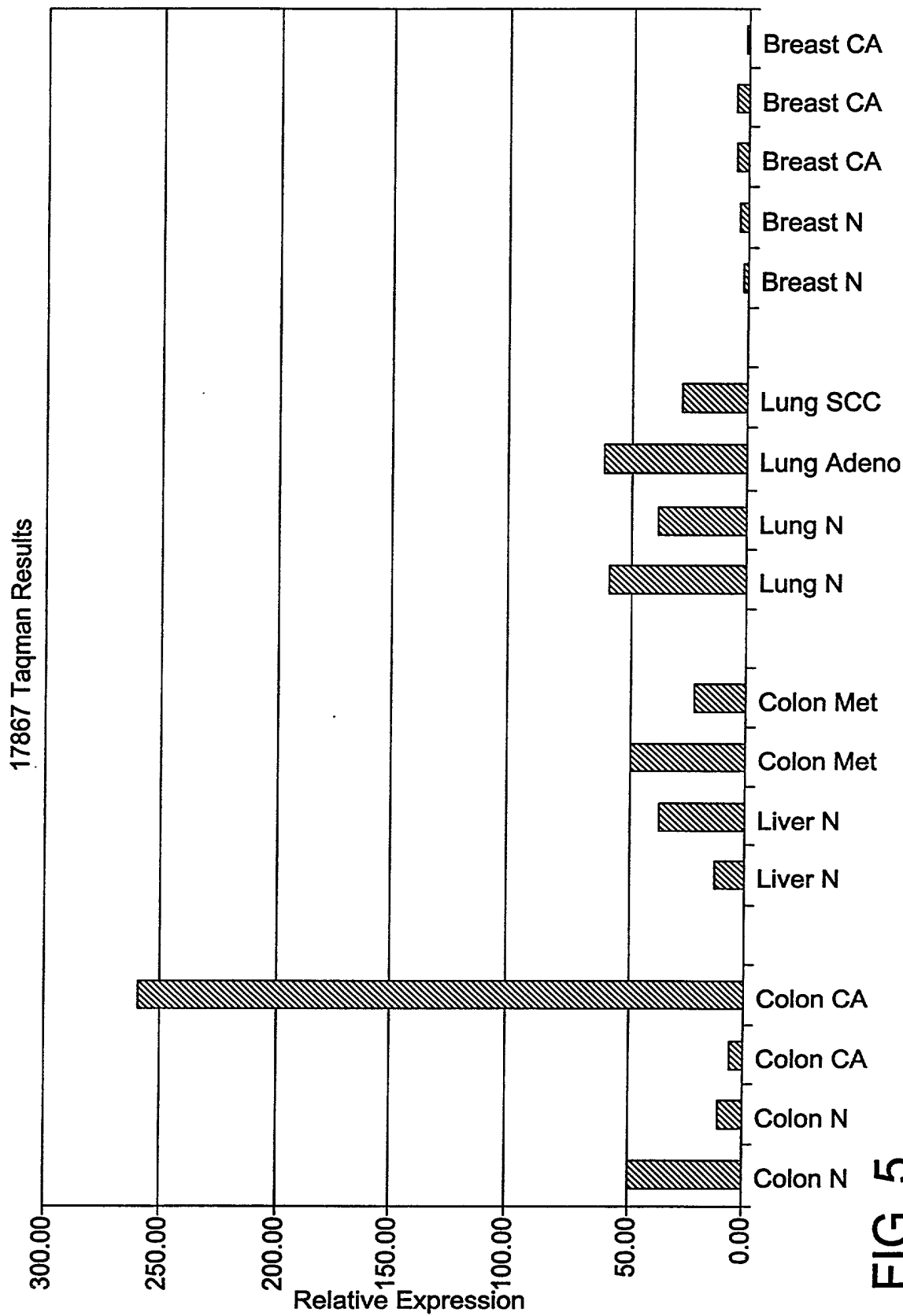


FIG. 5.

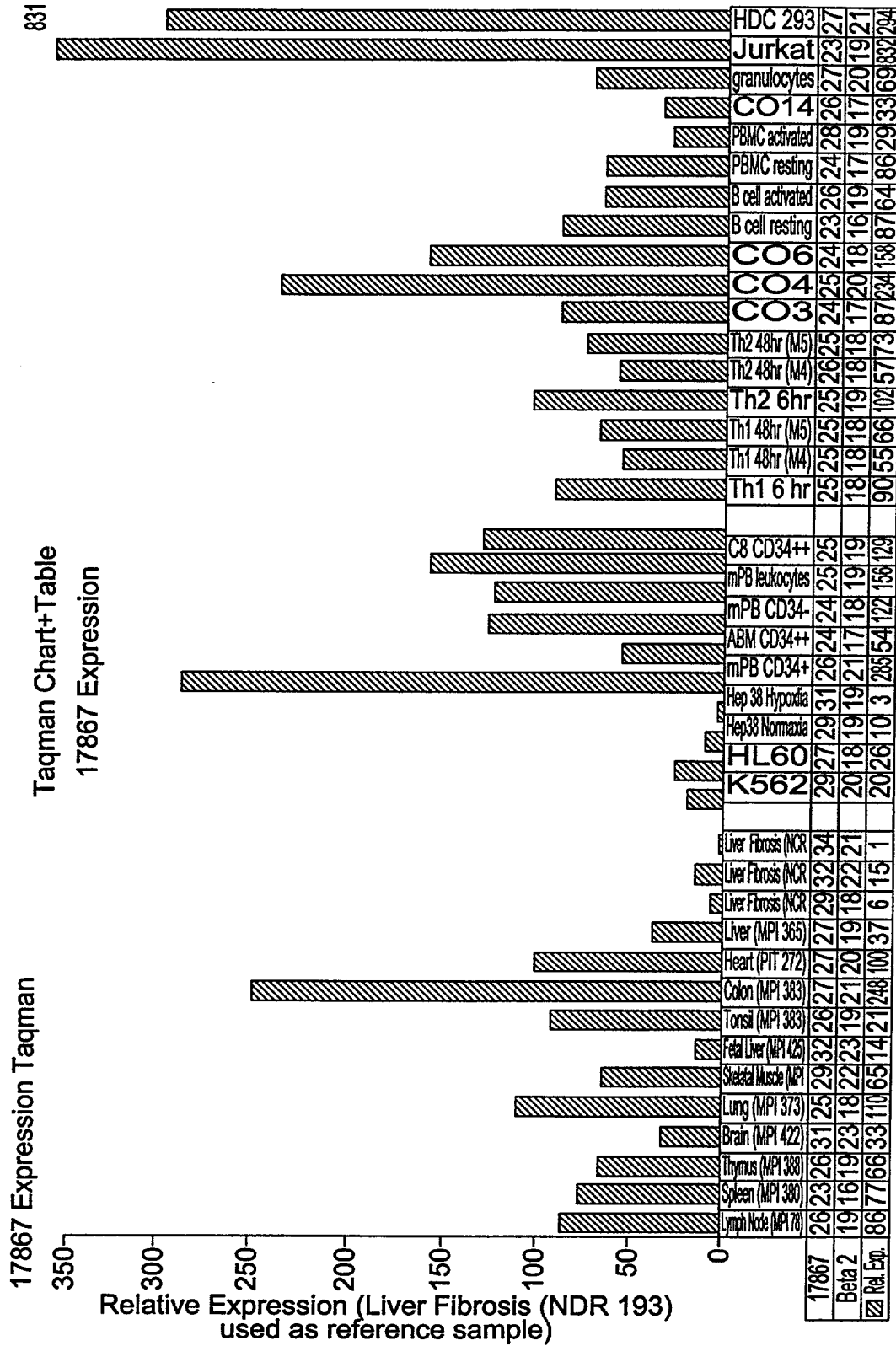


FIG. 6.